



## Sequence Listing

### SEQUENCE LISTING

#### (1) GENERAL INFORMATION:

(i) APPLICANT: Presta, Leonard G.  
Shelton, David L.  
Urfer, Roman

(ii) TITLE OF INVENTION: Human trk Receptors and Neurotrophic Factor Inhibitors

(iii) NUMBER OF SEQUENCES: 41

#### (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Knobbe, Martens, Olson & Bear  
(B) STREET: 620 Newport Center Drive 16th Floor  
(C) CITY: Newport Beach  
(D) STATE: California  
(E) COUNTRY: USA  
(F) ZIP: 92660

#### (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: WinPatin (Genentech)

#### (vi) CURRENT APPLICATION DATA

(A) APPLICATION NUMBER: 09/724,524  
(B) FILING DATE: 27-NOV-2000  
(C) CLASSIFICATION:

#### (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 09/156,923  
(B) FILING DATE: 18-SEP-1998  
(C) CLASSIFICATION:

#### (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/359,705  
(B) FILING DATE: 20-DEC-1994  
(C) CLASSIFICATION:

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#### (viii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/286846  
(B) FILING DATE: 10-AUG-1994

#### (viii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/215139  
(B) FILING DATE: 18-MAR-1994

#### (ix) ATTORNEY/AGENT INFORMATION:

(A) NAME: Dreger, Ginger  
(B) REGISTRATION NUMBER: 33,055  
(C) REFERENCE/DOCKET NUMBER: GENENT.33CP2C2

(x) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 949/760-0404

(B) TELEFAX: 949/760-9502

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3194 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGAAGGTTTA AAGAAGAAGC CGCAAAGCGC AGGGAAGGCC TCCCGGCACG 50  
GGTGGGGGAA AGCGGCCGGT GCAGCGCGGG GACAGGCACT CGGGCTGGCA 100  
CTGGCTGCTA GGGATGTCGT CCTGGATAAG GTGGCATGGA CCCGCCATGG 150  
CGCGGCTCTG GGGCTTCTGC TGGCTGGTTG TGGGCTTCTG GAGGGCCGCT 200  
TTCGCTGTC CCACGTCCTG CAAATGCAGT GCCTCTCGGA TCTGGTGCAG 250  
CGACCCTTCT CCTGGCATCG TGGCATTTC GAGATTGGAG CCTAACAGTG 300  
TAGATCCTGA GAACATCACC GAAATTTTCA TCGCAAACCA GAAAAGGTTA 350  
GAAATCATCA ACGAAGATGA TGTGAAGCT TATGTGGGAC TGAGAAATCT 400  
GACAATTGTG GATTCTGGAT TAAAATTTGT GGCTCATAAA GCATTTCTGA 450  
AAAACAGCAA CCTGCAGCAC ATCAATTTTA CCCGAAACAA ACTGACGAGT 500  
TTGTCTAGGA AACATTTCCG TCACCTTGAC TTGTCTGAAC TGATCCTGGT 550  
GGGCAATCCA TTTACATGCT CCTGTGACAT TATGTGGATC AAGACTCTCC 600  
AAGAGGCTAA ATCCAGTCCA GACACTCAGG ATTTGTACTG CCTGAATGAA 650  
AGCAGCAAGA ATATTCCCCT GGCAAACCTG CAGATACCCA ATTGTGGTTT 700  
GCCATCTGCA AATCTGGCCG CACCTAACCT CACTGTGGAG GAAGGAAAGT 750  
CTATCACATT ATCCTGTAGT GTGGCAGGTG ATCCGGTTCC TAATATGTAT 800  
TGGGATGTTG GTAACCTGGT TTCCAAACAT ATGAATGAAA CAAGCCACAC 850  
ACAGGGCTCC TTAAGGATAA CTAACATTTC ATCCGATGAC AGTGGGAAGC 900  
AGATCTCTTG TGTGGCGGAA AATCTTGTAG GAGAAGATCA AGATTCTGTC 950  
AACCTCACTG TGCATTTTGC ACCAACTATC ACATTTCTCG AATCTCCAAC 1000  
CTCAGACCAC CACTGGTGCA TTCCATTAC TGTGAAAGGC AACCCAAAAC 1050

CAGCGCTTCA GTGGTTCTAT AACGGGGCAA TATTGAATGA GTCCAAATAC 1100  
ATCTGTACTA AAATACATGT TACCAATCAC ACGGAGTACC ACGGCTGCCT 1150  
CCAGCTGGAT AATCCCACTC ACATGAACAA TGGGGACTAC ACTCTAATAG 1200  
CCAAGAATGA GTATGGGAAG GATGAGAAAC AGATTTCTGC TCACTTCATG 1250  
GGCTGGCCTG GAATTGACGA TGGTGCAAAC CCAAATTATC CTGATGTAAT 1300  
TTATGAAGAT TATGGAAGT CAGCGAATGA CATCGGGGAC ACCACGAACA 1350  
GAAGTAATGA AATCCCTTCC ACAGACGTCA CTGATAAAAC CGGTCGGGAA 1400  
CATCTCTCGG TCTATGCTGT GGTGGTGATT GCGTCTGTGG TGGGATTTTG 1450  
CCTTTTGGTA ATGCTGTTTC TGCTTAAGTT GGCAAGACAC TCCAAGTTTG 1500  
GCATGAAAGG CCCAGCCTCC GTTATCAGCA ATGATGATGA CTCTGCCAGC 1550  
CCACTCCATC ACATCTCCAA TGGGAGTAAC ACTCCATCTT CTTCGGAAGG 1600  
TGGCCCAGAT GCTGTCATTA TTGGAATGAC CAAGATCCCT GTCATTGAAA 1650  
ATCCCCAGTA CTTTGGCATC ACCAACAGTC AGCTCAAGCC AGACACATTT 1700  
GTTCAGCACA TCAAGCGACA TAACATTGTT CTGAAAAGGG AGCTAGGCGA 1750  
AGGAGCCTTT GGAAAAGTGT TCCTAGCTGA ATGCTATAAC CTCTGTCCTG 1800  
AGCAGGACAA GATCTTGGTG GCAGTGAAGA CCCTGAAGGA TGCCAGTGAC 1850  
AATGCACGCA AGGACTTCCA CCGTGAGGCC GAGCTCCTGA CCAACCTCCA 1900  
GCATGAGCAC ATCGTCAAGT TCTATGGCGT CTGCGTGGAG GGCGACCCCC 1950  
TCATCATGGT CTTTGAGTAC ATGAAGCATG GGGACCTCAA CAAGTTCCTC 2000  
AGGGCACACG GCCCTGATGC CGTGCTGATG GCTGAGGGCA ACCCGCCCAC 2050  
GGAAGTACG CAGTCGCAGA TGCTGCATAT AGCCCAGCAG ATCGCCGCGG 2100  
GCATGGTCTA CCTGGCGTCC CAGCACTTCG TGCAACGCGA TTTGGCCACC 2150  


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AGGAACTGCC TGGTCGGGGA GAACTTGCTG GTGAAAATCG GGGACTTTGG 2200  
GATGTCCCGG GACGTGTACA GCACTGACTA CTACAGGGTC GGTGGCCACA 2250  
CAATGCTGCC CATTCGCTGG ATGCCTCCAG AGAGCATCAT GTACAGGAAA 2300  
TTCACGACGG AAAGCGACGT CTGGAGCCTG GGGGTCGTGT TGTGGGAGAT 2350  
TTTCACCTAT GGCAAACAGC CCTGGTACCA GCTGTCAAAC AATGAGGTGA 2400  
TAGAGTGTAT CACTCAGGGC CGAGTCCTGC AGCGACCCCG CACGTGCCCC 2450  
CAGGAGGTGT ATGAGCTGAT GCTGGGGTGC TGGCAGCGAG AGCCCCACAT 2500

GAGGAAGAAC ATCAAGGGCA TCCATACCCT CCTTCAGAAC TTGGCCAAGG 2550  
CATCTCCGGT CTACCTGGAC ATTCTAGGCT AGGGCCCTTT TCCCCAGACC 2600  
GATCCTTCCC AACGTACTCC TCAGACGGGC TGAGAGGATG AACATCTTTT 2650  
AACTGCCGCT GGAGGCCACC AAGCTGCTCT CCTTCACTCT GACAGTATTA 2700  
ACATCAAAGA CTCCGAGAAG CTCTCGAGGG AAGCAGTGTG TACTTCTTCA 2750  
TCCATAGACA CAGTATTGAC TTCTTTTTTG CATTATCTCT TTCTCTCTTT 2800  
CCATCTCCCT TGGTTGTTCC TTTTCTTTT TTTAAATTTT CTTTTCTTC 2850  
TTTTTTTTCG TCTTCCCTGC TTCACGATTC TTACCCTTTC TTTTGAATCA 2900  
ATCTGGCTTC TGCATTACTA TTAACCTGTC ATAGACAAAG GCCTTAACAA 2950  
ACGTAATTTG TTATATCAGC AGACACTCCA GTTTGCCCCAC CACAACAAAC 3000  
AATGCCTTGT TGTATTCCTG CCTTTGATGT GGATGAAAAA AAGGGAAAAAC 3050  
AAATATTTCA CTAAACTTT GTCACCTCTG CTGTACAGAT ATCGAGAGTT 3100  
TCTATGGATT CACTTCTATT TATTTATTAT TATTACTGTT CTTATTGTTT 3150  
TTGGATGGCT TAAGCCTGTG TATAAAAAA AAAAAAATC TAGA 3194

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ser	Ser	Trp	Ile	Arg	Trp	His	Gly	Pro	Ala	Met	Ala	Arg	Leu
1				5					10					15
Trp	Gly	Phe	Cys	Trp	Leu	Val	Val	Gly	Phe	Trp	Arg	Ala	Ala	Phe
			20						25					30
Ala	Cys	Pro	Thr	Ser	Cys	Lys	Cys	Ser	Ala	Ser	Arg	Ile	Trp	Cys
				35					40					45
Ser	Asp	Pro	Ser	Pro	Gly	Ile	Val	Ala	Phe	Pro	Arg	Leu	Glu	Pro
				50					55					60
Asn	Ser	Val	Asp	Pro	Glu	Asn	Ile	Thr	Glu	Ile	Phe	Ile	Ala	Asn
				65					70					75
Gln	Lys	Arg	Leu	Glu	Ile	Ile	Asn	Glu	Asp	Asp	Val	Glu	Ala	Tyr
				80					85					90
Val	Gly	Leu	Arg	Asn	Leu	Thr	Ile	Val	Asp	Ser	Gly	Leu	Lys	Phe

	95	100	105
Val Ala His Lys	Ala Phe Leu Lys Asn Ser Asn Leu Gln His Ile		
	110	115	120
Asn Phe Thr Arg	Asn Lys Leu Thr Ser Leu Ser Arg Lys His Phe		
	125	130	135
Arg His Leu Asp	Leu Ser Glu Leu Ile Leu Val Gly Asn Pro Phe		
	140	145	150
Thr Cys Ser Cys	Asp Ile Met Trp Ile Lys Thr Leu Gln Glu Ala		
	155	160	165
Lys Ser Ser Pro	Asp Thr Gln Asp Leu Tyr Cys Leu Asn Glu Ser		
	170	175	180
Ser Lys Asn Ile	Pro Leu Ala Asn Leu Gln Ile Pro Asn Cys Gly		
	185	190	195
Leu Pro Ser Ala	Asn Leu Ala Ala Pro Asn Leu Thr Val Glu Glu		
	200	205	210
Gly Lys Ser Ile	Thr Leu Ser Cys Ser Val Ala Gly Asp Pro Val		
	215	220	225
Pro Asn Met Tyr	Trp Asp Val Gly Asn Leu Val Ser Lys His Met		
	230	235	240
Asn Glu Thr Ser	His Thr Gln Gly Ser Leu Arg Ile Thr Asn Ile		
	245	250	255
Ser Ser Asp Asp	Ser Gly Lys Gln Ile Ser Cys Val Ala Glu Asn		
	260	265	270
Leu Val Gly Glu	Asp Gln Asp Ser Val Asn Leu Thr Val His Phe		
	275	280	285
Ala Pro Thr Ile	Thr Phe Leu Glu Ser Pro Thr Ser Asp His His		
	290	295	300
Trp Cys Ile Pro	Phe Thr Val Lys Gly Asn Pro Lys Pro Ala Leu		
	305	310	315

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Gln Trp Phe Tyr	Asn Gly Ala Ile Leu Asn Glu Ser Lys Tyr Ile		
	320	325	330
Cys Thr Lys Ile	His Val Thr Asn His Thr Glu Tyr His Gly Cys		
	335	340	345
Leu Gln Leu Asp	Asn Pro Thr His Met Asn Asn Gly Asp Tyr Thr		
	350	355	360
Leu Ile Ala Lys	Asn Glu Tyr Gly Lys Asp Glu Lys Gln Ile Ser		
	365	370	375
Ala His Phe Met	Gly Trp Pro Gly Ile Asp Asp Gly Ala Asn Pro		

	380		385		390
Asn Tyr Pro Asp	Val Ile Tyr Glu Asp	Tyr Gly Thr Ala Ala	Asn		
	395		400		405
Asp Ile Gly Asp	Thr Thr Asn Arg Ser	Asn Glu Ile Pro Ser	Thr		
	410		415		420
Asp Val Thr Asp	Lys Thr Gly Arg Glu	His Leu Ser Val Tyr	Ala		
	425		430		435
Val Val Val Ile	Ala Ser Val Val Gly	Phe Cys Leu Leu Val	Met		
	440		445		450
Leu Phe Leu Leu	Lys Leu Ala Arg His	Ser Lys Phe Gly Met	Lys		
	455		460		465
Gly Pro Ala Ser	Val Ile Ser Asn Asp	Asp Asp Ser Ala Ser	Pro		
	470		475		480
Leu His His Ile	Ser Asn Gly Ser Asn	Thr Pro Ser Ser Ser	Glu		
	485		490		495
Gly Gly Pro Asp	Ala Val Ile Ile Gly	Met Thr Lys Ile Pro	Val		
	500		505		510
Ile Glu Asn Pro	Gln Tyr Phe Gly Ile	Thr Asn Ser Gln Leu	Lys		
	515		520		525
Pro Asp Thr Phe	Val Gln His Ile Lys	Arg His Asn Ile Val	Leu		
	530		535		540
Lys Arg Glu Leu	Gly Glu Gly Ala Phe	Gly Lys Val Phe Leu	Ala		
	545		550		555
Glu Cys Tyr Asn	Leu Cys Pro Glu Gln	Asp Lys Ile Leu Val	Ala		
	560		565		570
Val Lys Thr Leu	Lys Asp Ala Ser Asp	Asn Ala Arg Lys Asp	Phe		
	575		580		585
His Arg Glu Ala	Glu Leu Leu Thr Asn	Leu Gln His Glu His	Ile		
	590		595		600

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Val Lys Phe Tyr	Gly Val Cys Val Glu	Gly Asp Pro Leu Ile	Met		
	605		610		615
Val Phe Glu Tyr	Met Lys His Gly Asp	Leu Asn Lys Phe Leu	Arg		
	620		625		630
Ala His Gly Pro	Asp Ala Val Leu Met	Ala Glu Gly Asn Pro	Pro		
	635		640		645
Thr Glu Leu Thr	Gln Ser Gln Met Leu	His Ile Ala Gln Gln	Ile		
	650		655		660
Ala Ala Gly Met	Val Tyr Leu Ala Ser	Gln His Phe Val His	Arg		

665	670	675
Asp Leu Ala Thr Arg Asn Cys Leu Val Gly Glu Asn Leu Leu Val		
680	685	690
Lys Ile Gly Asp Phe Gly Met Ser Arg Asp Val Tyr Ser Thr Asp		
695	700	705
Tyr Tyr Arg Val Gly Gly His Thr Met Leu Pro Ile Arg Trp Met		
710	715	720
Pro Pro Glu Ser Ile Met Tyr Arg Lys Phe Thr Thr Glu Ser Asp		
725	730	735
Val Trp Ser Leu Gly Val Val Leu Trp Glu Ile Phe Thr Tyr Gly		
740	745	750
Lys Gln Pro Trp Tyr Gln Leu Ser Asn Asn Glu Val Ile Glu Cys		
755	760	765
Ile Thr Gln Gly Arg Val Leu Gln Arg Pro Arg Thr Cys Pro Gln		
770	775	780
Glu Val Tyr Glu Leu Met Leu Gly Cys Trp Gln Arg Glu Pro His		
785	790	795
Met Arg Lys Asn Ile Lys Gly Ile His Thr Leu Leu Gln Asn Leu		
800	805	810
Ala Lys Ala Ser Pro Val Tyr Leu Asp Ile Leu Gly		
815	820	822

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1870 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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GGAAGGTTTA AAGAAGAAGC CGCAAAGCGC AGGGAAGGCC TCCCGGCACG 50

GGTGGGGGAA AGCGGCCGGT GCAGCGCGGG GACAGGCACT CGGGCTGGCA 100

CTGGCTGCTA GGGATGTCGT CCTGGATAAG GTGGCATGGA CCCGCCATGG 150

CGCGGCTCTG GGGCTTCTGC TGGCTGGTTG TGGGCTTCTG GAGGGCCGCT 200

TTCGCCTGTC CCACGTCTG CAAATGCAGT GCCTCTCGGA TCTGGTGCAG 250

CGACCCTTCT CCTGGCATCG TGGCATTTC GAGATTGGAG CCTAACAGTG 300

TAGATCCTGA GAACATCACC GAAATTTTCA TCGCAAACCA GAAAAGGTTA 350

GAAATCATCA ACGAAGATGA TGTTGAAGCT TATGTGGGAC TGAGAAATCT 400  
 GACAATTGTG GATTCTGGAT TAAAATTTGT GGCTCATAAA GCATTTCTGA 450  
 AAAACAGCAA CCTGCAGCAC ATCAATTTTA CCCGAAACAA ACTGACGAGT 500  
 TTGTCTAGGA AACATTTCCG TCACCTTGAC TTGTCTGAAC TGATCCTGGT 550  
 GGGCAATCCA TTTACATGCT CCTGTGACAT TATGTGGATC AAGACTCTCC 600  
 AAGAGGCTAA ATCCAGTCCA GACACTCAGG ATTTGTACTG CCTGAATGAA 650  
 AGCAGCAAGA ATATTCCCCT GGCAAACCTG CAGATACCCA ATTGTGGTTT 700  
 GCCATCTGCA AATCTGGCCG CACCTAACCT CACTGTGGAG GAAGGAAAGT 750  
 CTATCACATT ATCCTGTAGT GTGGCAGGTG ATCCGGTTCC TAATATGTAT 800  
 TGGGATGTTG GTAACCTGGT TTCCAAACAT ATGAATGAAA CAAGCCACAC 850  
 ACAGGGCTCC TTAAGGATAA CTAACATTTC ATCCGATGAC AGTGGGAAGC 900  
 AGATCTCTTG TGTGGCGGAA AATCTTGTAG GAGAAGATCA AGATTCTGTC 950  
 AACCTCACTG TGCATTTTGC ACCAACTATC ACATTTCTCG AATCTCCAAC 1000  
 CTCAGACCAC CACTGGTGCA TTCCATTAC TGTGAAAGGC AACCCAAAAC 1050  
 CAGCGCTTCA GTGGTTCTAT AACGGGGCAA TATTGAATGA GTCCAAATAC 1100  
 ATCTGTACTA AAATACATGT TACCAATCAC ACGGAGTACC ACGGCTGCCT 1150  
 CCAGCTGGAT AATCCCCTC ACATGAACAA TGGGGACTAC ACTCTAATAG 1200  
 CCAAGAATGA GTATGGGAAG GATGAGAAAC AGATTTCTGC TCACTTCATG 1250  
 GGCTGGCCTG GAATTGACGA TGGTGCAAAC CCAAATTATC CTGATGTAAT 1300  
 TTATGAAGAT TATGGAAGT CAGCGAATGA CATCGGGGAC ACCACGAACA 1350  
 GAAGTAATGA AATCCCTTCC ACAGACGTCA CTGATAAAAC CGGTCGGGAA 1400  
 CATCTCTCGG TCTATGCTGT GGTGGTGATT GCGTCTGTGG TGGGATTTTG 1450  


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 CCTTTTGGTA ATGCTGTTTC TGCTTAAGTT GGCAAGACAC TCCAAGTTTG 1500  
 GCATGAAAGG TTTTGTTTTG TTTCATAAGA TCCCACTGGA TGGGTAGCTG 1550  
 AAATAAGGA AAAGACAGAG AAAGGGGCTG TGGTGCTTGT TGGTTGATGC 1600  
 TGCCATGTAA GCTGGACTCC TGGGACTGCT GTTGGCTTAT CCCGGGAAGT 1650  
 GCTGCTTATC TGGGGTTTTT TGGTAGATGT GGGCGGTGTT TGGAGGCTGT 1700  
 ACTATATGAA GCCTGCATAT ACTGTGAGCT GTGATTGGGG AACACCAATG 1750  
 CAGAGGTAAC TCTCAGGCAG CTAAGCAGCA CCTCAAGAAA ACATGTTAAA 1800



TTAATGCTTC TCTTCTTACA GTAGTTCAAA TACAAAAC TG AAATGAAATC 1850

CCATTGGATT GTACTTCTCT 1870

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 477 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ser Ser Trp Ile Arg Trp His Gly Pro Ala Met Ala Arg Leu  
1 5 10 15

Trp Gly Phe Cys Trp Leu Val Val Gly Phe Trp Arg Ala Ala Phe  
20 25 30

Ala Cys Pro Thr Ser Cys Lys Cys Ser Ala Ser Arg Ile Trp Cys  
35 40 45

Ser Asp Pro Ser Pro Gly Ile Val Ala Phe Pro Arg Leu Glu Pro  
50 55 60

Asn Ser Val Asp Pro Glu Asn Ile Thr Glu Ile Phe Ile Ala Asn  
65 70 75

Gln Lys Arg Leu Glu Ile Ile Asn Glu Asp Asp Val Glu Ala Tyr  
80 85 90

Val Gly Leu Arg Asn Leu Thr Ile Val Asp Ser Gly Leu Lys Phe  
95 100 105

Val Ala His Lys Ala Phe Leu Lys Asn Ser Asn Leu Gln His Ile  
110 115 120

Asn Phe Thr Arg Asn Lys Leu Thr Ser Leu Ser Arg Lys His Phe  
125 130 135

Arg His Leu Asp Leu Ser Glu Leu Ile Leu Val Gly Asn Pro Phe  
140 145 150

Thr Cys Ser Cys Asp Ile Met Trp Ile Lys Thr Leu Gln Glu Ala  
155 160 165

Lys Ser Ser Pro Asp Thr Gln Asp Leu Tyr Cys Leu Asn Glu Ser  
170 175 180

Ser Lys Asn Ile Pro Leu Ala Asn Leu Gln Ile Pro Asn Cys Gly  
185 190 195

Leu Pro Ser Ala Asn Leu Ala Ala Pro Asn Leu Thr Val Glu Glu  
200 205 210

Gly Lys Ser Ile Thr Leu Ser Cys Ser Val Ala Gly Asp Pro Val

215	220	225
Pro Asn Met Tyr Trp Asp Val Gly Asn Leu Val Ser Lys His Met		
230	235	240
Asn Glu Thr Ser His Thr Gln Gly Ser Leu Arg Ile Thr Asn Ile		
245	250	255
Ser Ser Asp Asp Ser Gly Lys Gln Ile Ser Cys Val Ala Glu Asn		
260	265	270
Leu Val Gly Glu Asp Gln Asp Ser Val Asn Leu Thr Val His Phe		
275	280	285
Ala Pro Thr Ile Thr Phe Leu Glu Ser Pro Thr Ser Asp His His		
290	295	300
Trp Cys Ile Pro Phe Thr Val Lys Gly Asn Pro Lys Pro Ala Leu		
305	310	315
Gln Trp Phe Tyr Asn Gly Ala Ile Leu Asn Glu Ser Lys Tyr Ile		
320	325	330
Cys Thr Lys Ile His Val Thr Asn His Thr Glu Tyr His Gly Cys		
335	340	345
Leu Gln Leu Asp Asn Pro Thr His Met Asn Asn Gly Asp Tyr Thr		
350	355	360
Leu Ile Ala Lys Asn Glu Tyr Gly Lys Asp Glu Lys Gln Ile Ser		
365	370	375
Ala His Phe Met Gly Trp Pro Gly Ile Asp Asp Gly Ala Asn Pro		
380	385	390
Asn Tyr Pro Asp Val Ile Tyr Glu Asp Tyr Gly Thr Ala Ala Asn		
395	400	405
Asp Ile Gly Asp Thr Thr Asn Arg Ser Asn Glu Ile Pro Ser Thr		
410	415	420
Asp Val Thr Asp Lys Thr Gly Arg Glu His Leu Ser Val Tyr Ala		
425	430	435
Val Val Val Ile Ala Ser Val Val Gly Phe Cys Leu Leu Val Met		
440	445	450
Leu Phe Leu Leu Lys Leu Ala Arg His Ser Lys Phe Gly Met Lys		
455	460	465
Gly Phe Val Leu Phe His Lys Ile Pro Leu Asp Gly		
470	475	477

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2715 base pairs

(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGATCCGCGT CGGAGATGGA TGTCTCTCTT TGCCCAGCCA AGTGTAGTTT 50  
CTGGCGGATT TTCTTGCTGG GAAGCGTCTG GCTGGACTAT GTGGGCTCCG 100  
TGCTGGCTTG CCCTGCAAAT TGTGTCTGCA GCAAGACTGA GATCAATTGC 150  
CGGCGGCCGG ACGATGGGAA CCTCTTCCCC CTCCTGGAAG GGCAGGATTC 200  
AGGGAACAGC AATGGGAACG CCAATATCAA CATCACGGAC ATCTCAAGGA 250  
ATATCACTTC CATAACATA GAGAACTGGC GCAGTCTTCA CACGCTCAAC 300  
GCCGTGGACA TGGAGCTCTA CACCGGACTT CAAAAGCTGA CCATCAAGAA 350  
CTCAGGACTT CGGAGCATTG AGCCCAGAGC CTTTGCCAAG AACCCCCATT 400  
TGC GTTATAT AAACCTGTCA AGTAACCGGC TCACCACACT CTCGTGGCAG 450  
CTCTTCCAGA CGCTGAGTCT TCGGGAATTG CAGTTGGAGC AGAACTTTTT 500  
CAACTGCAGC TGTGACATCC GCTGGATGCA GCTCTGGCAG GAGCAGGGGG 550  
AGGCCAAGCT CAACAGCCAG AACCTCTACT GCATCAATGC TGATGGCTCC 600  
CAGCTTCCTC TCTTCCGCAT GAACATCAGT CAGTGTGACC TTCCTGAGAT 650  
CAGCGTGAGC CACGTCAACC TGACCGTACG AGAGGGTGAC AATGCTGTTA 700  
TCACTTGCAA TGGCTCTGGA TCACCCCTTC CTGATGTGGA CTGGATAGTC 750  
ACTGGGCTGC AGTCCATCAA CACTCACCAG ACCAATCTGA ACTGGACCAA 800  
TGTTCATGCC ATCAACTTGA CGCTGGTGAA TGTGACGAGT GAGGACAATG 850  
GCTTACCCTT GACGTGCATT GCAGAGAACG TGGTGGGCAT GAGCAATGCC 900  
AGTGTGCCCC TCACTGTCTA CTATCCCCCA CGTGTGGTGA GCCTGGAGGA 950  
GCCTGAGCTG CGCCTGGAGC ACTGCATCGA GTTTGTGGTG CGTGGCAACC 1000  
CCCCACCAAC GCTGCACTGG CTGCACAATG GGCAGCCTCT GCGGGAGTCC 1050  
AAGATCATCC ATGTGGAATA CTACCAAGAG GGAGAGATTT CCGAGGGCTG 1100  
CCTGCTCTTC AACAAGCCCA CCCACTACAA CAATGGCAAC TATACCCTCA 1150  
TTGCCAAAAA CCCACTGGGC ACAGCCAACC AGACCATCAA TGGCCACTTC 1200  
CTCAAGGAGC CCTTTCAGA GAGCACGGAT AACTTTATCT TGTTTGACGA 1250

AGTGAGTCCC ACACCTCCTA TCACTGTGAC CCACAAACCA GAAGAAGACA 1300  
 CTTTTGGGGT ATCCATAGCA GTTGGACTTG CTGCTTTTGC CTGTGTCCTG 1350  
 TTGGTGGTTC TCTTCGTCAT GATCAACAAA TATGGTCGAC GGTCCAAATT 1400  
 TGGAATGAAG GGTCCCCTGG CTGTCATCAG TGGTGAGGAG GACTCAGCCA 1450  
 GCCCACTGCA CCACATCAAC CACGGCATCA CCACGCCCTC GTCACTGGAT 1500  
 GCCGGGCCCCG ACACTGTGGT CATTGGCATG ACTCGCATCC CTGTCATTGA 1550  
 GAACCCCCAG TACTTCCGTC AGGGACACAA CTGCCACAAG CCGGACACGT 1600  
 ATGTGCAGCA CATTAAGAGG AGAGACATCG TGCTGAAGCG AGAACTGGGT 1650  
 GAGGGAGCCT TTGGAAAGGT CTCCTGGCC GAGTGCTACA ACCTCAGCCC 1700  
 GACCAAGGAC AAGATGCTTG TGGCTGTGAA GGCCCTGAAG GATCCCACCC 1750  
 TGGGTGCCCCG GAAGGATTTC CAGAGGGAGG CCGAGCTGCT CACCAACCTG 1800  
 CAGCATGAGC ACATTGTCAA GTTCTATGGA GTGTGCGGCG ATGGGGACCC 1850  
 CCTCATCATG GTCTTTGAAT ACATGAAGCA TGGAGACCTG AATAAGTTCC 1900  
 TCAGGGCCCA TGGGCCAGAT GCAATGATCC TTGTGGATGG ACAGCCACGC 1950  
 CAGGCCAAGG GTGAGCTGGG GCTCTCCCAA ATGCTCCACA TTGCCAGTCA 2000  
 GATCGCCTCG GGTATGGTGT ACCTGGCCTC CCAGCACTTT GTGCACCGAG 2050  
 ACCTGGCCAC CAGGAACTGC CTGGTTGGAG CGAATCTGCT AGTGAAGATT 2100  
 GGGGACTTCG GCATGTCCAG AGATGTCTAC AGCACGGATT ATTACAGGCT 2150  
 CTTTAATCCA TCTGGAAATG ATTTTGTAT ATGGTGTGAG GTGGGAGGAC 2200  
 ACACCATGCT CCCCATTCGC TGGATGCCTC CTGAAAGCAT CATGTACCGG 2250  
 AAGTTCACTA CAGAGAGTGA TGTATGGAGC TTCGGGGTGA TCCTCTGGGA 2300  
 GATCTTCACC TATGGAAAGC AGCCATGGTT CCAACTCTCA AACACGGAGG 2350

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TCATTGAGTG CATTACCCAA GGTCGTGTTT TGGAGCGGCC CCGAGTCTGC 2400  
 CCCAAAGAGG TGTACGATGT CATGCTGGGG TGCTGGCAGA GGGAAACCACA 2450  
 GCAGCGGTTG AACATCAAGG AGATCTACAA AATCCTCCAT GCTTTGGGGA 2500  
 AGGCCACCCC AATCTACCTG GACATTCTTG GCTAGTGGTG GCTGGTGGTC 2550  
 ATGAATTCAT ACTCTGTTGC CTCCTCTCTC CCTGCCTCAC ATCTCCCTTC 2600  
 CACCTCACAA CTCCTTCCAT CCTTGACTGA AGCGAACATC TTCATATAAA 2650  
 CTCAAGTGCC TGCTACACAT ACAACACTGA AAAAAGGAAA AAAAAAGAAA 2700

AAAAAAAAAA ACCGC 2715

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 839 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Asp	Val	Ser	Leu	Cys	Pro	Ala	Lys	Cys	Ser	Phe	Trp	Arg	Ile	
1				5					10					15	
Phe	Leu	Leu	Gly	Ser	Val	Trp	Leu	Asp	Tyr	Val	Gly	Ser	Val	Leu	
				20					25					30	
Ala	Cys	Pro	Ala	Asn	Cys	Val	Cys	Ser	Lys	Thr	Glu	Ile	Asn	Cys	
				35					40					45	
Arg	Arg	Pro	Asp	Asp	Gly	Asn	Leu	Phe	Pro	Leu	Leu	Glu	Gly	Gln	
				50					55					60	
Asp	Ser	Gly	Asn	Ser	Asn	Gly	Asn	Ala	Asn	Ile	Asn	Ile	Thr	Asp	
				65					70					75	
Ile	Ser	Arg	Asn	Ile	Thr	Ser	Ile	His	Ile	Glu	Asn	Trp	Arg	Ser	
				80					85					90	
Leu	His	Thr	Leu	Asn	Ala	Val	Asp	Met	Glu	Leu	Tyr	Thr	Gly	Leu	
				95					100					105	
Gln	Lys	Leu	Thr	Ile	Lys	Asn	Ser	Gly	Leu	Arg	Ser	Ile	Gln	Pro	
				110					115					120	
Arg	Ala	Phe	Ala	Lys	Asn	Pro	His	Leu	Arg	Tyr	Ile	Asn	Leu	Ser	
				125					130					135	
Ser	Asn	Arg	Leu	Thr	Thr	Leu	Ser	Trp	Gln	Leu	Phe	Gln	Thr	Leu	
				140					145					150	
Ser	Leu	Arg	Glu	Leu	Gln	Leu	Glu	Gln	Asn	Phe	Phe	Asn	Cys	Ser	
				155					160					165	
Cys	Asp	Ile	Arg	Trp	Met	Gln	Leu	Trp	Gln	Glu	Gln	Gly	Glu	Ala	
				170					175					180	
Lys	Leu	Asn	Ser	Gln	Asn	Leu	Tyr	Cys	Ile	Asn	Ala	Asp	Gly	Ser	
				185					190					195	
Gln	Leu	Pro	Leu	Phe	Arg	Met	Asn	Ile	Ser	Gln	Cys	Asp	Leu	Pro	
				200					205					210	
Glu	Ile	Ser	Val	Ser	His	Val	Asn	Leu	Thr	Val	Arg	Glu	Gly	Asp	
				215					220					225	

Asn	Ala	Val	Ile	Thr	Cys	Asn	Gly	Ser	Gly	Ser	Pro	Leu	Pro	Asp	
				230					235					240	
Val	Asp	Trp	Ile	Val	Thr	Gly	Leu	Gln	Ser	Ile	Asn	Thr	His	Gln	
				245					250					255	
Thr	Asn	Leu	Asn	Trp	Thr	Asn	Val	His	Ala	Ile	Asn	Leu	Thr	Leu	
				260					265					270	
Val	Asn	Val	Thr	Ser	Glu	Asp	Asn	Gly	Phe	Thr	Leu	Thr	Cys	Ile	
				275					280					285	
Ala	Glu	Asn	Val	Val	Gly	Met	Ser	Asn	Ala	Ser	Val	Ala	Leu	Thr	
				290					295					300	
Val	Tyr	Tyr	Pro	Pro	Arg	Val	Val	Ser	Leu	Glu	Glu	Pro	Glu	Leu	
				305					310					315	
Arg	Leu	Glu	His	Cys	Ile	Glu	Phe	Val	Val	Arg	Gly	Asn	Pro	Pro	
				320					325					330	
Pro	Thr	Leu	His	Trp	Leu	His	Asn	Gly	Gln	Pro	Leu	Arg	Glu	Ser	
				335					340					345	
Lys	Ile	Ile	His	Val	Glu	Tyr	Tyr	Gln	Glu	Gly	Glu	Ile	Ser	Glu	
				350					355					360	
Gly	Cys	Leu	Leu	Phe	Asn	Lys	Pro	Thr	His	Tyr	Asn	Asn	Gly	Asn	
				365					370					375	
Tyr	Thr	Leu	Ile	Ala	Lys	Asn	Pro	Leu	Gly	Thr	Ala	Asn	Gln	Thr	
				380					385					390	
Ile	Asn	Gly	His	Phe	Leu	Lys	Glu	Pro	Phe	Pro	Glu	Ser	Thr	Asp	
				395					400					405	
Asn	Phe	Ile	Leu	Phe	Asp	Glu	Val	Ser	Pro	Thr	Pro	Pro	Ile	Thr	
				410					415					420	
Val	Thr	His	Lys	Pro	Glu	Glu	Asp	Thr	Phe	Gly	Val	Ser	Ile	Ala	
				425					430					435	
Val	Gly	Leu	Ala	Ala	Phe	Ala	Cys	Val	Leu	Leu	Val	Val	Leu	Phe	
				440					445					450	
Val	Met	Ile	Asn	Lys	Tyr	Gly	Arg	Arg	Ser	Lys	Phe	Gly	Met	Lys	
				455					460					465	
Gly	Pro	Val	Ala	Val	Ile	Ser	Gly	Glu	Glu	Asp	Ser	Ala	Ser	Pro	
				470					475					480	
Leu	His	His	Ile	Asn	His	Gly	Ile	Thr	Thr	Pro	Ser	Ser	Leu	Asp	
				485					490					495	
Ala	Gly	Pro	Asp	Thr	Val	Val	Ile	Gly	Met	Thr	Arg	Ile	Pro	Val	
				500					505					510	

Ile Glu Asn Pro Gln Tyr Phe Arg Gln Gly His Asn Cys His Lys  
515 520 525

Pro Asp Thr Tyr Val Gln His Ile Lys Arg Arg Asp Ile Val Leu  
530 535 540

Lys Arg Glu Leu Gly Glu Gly Ala Phe Gly Lys Val Phe Leu Ala  
545 550 555

Glu Cys Tyr Asn Leu Ser Pro Thr Lys Asp Lys Met Leu Val Ala  
560 565 570

Val Lys Ala Leu Lys Asp Pro Thr Leu Ala Ala Arg Lys Asp Phe  
575 580 585

Gln Arg Glu Ala Glu Leu Leu Thr Asn Leu Gln His Glu His Ile  
590 595 600

Val Lys Phe Tyr Gly Val Cys Gly Asp Gly Asp Pro Leu Ile Met  
605 610 615

Val Phe Glu Tyr Met Lys His Gly Asp Leu Asn Lys Phe Leu Arg  
620 625 630

Ala His Gly Pro Asp Ala Met Ile Leu Val Asp Gly Gln Pro Arg  
635 640 645

Gln Ala Lys Gly Glu Leu Gly Leu Ser Gln Met Leu His Ile Ala  
650 655 660

Ser Gln Ile Ala Ser Gly Met Val Tyr Leu Ala Ser Gln His Phe  
665 670 675

Val His Arg Asp Leu Ala Thr Arg Asn Cys Leu Val Gly Ala Asn  
680 685 690

Leu Leu Val Lys Ile Gly Asp Phe Gly Met Ser Arg Asp Val Tyr  
695 700 705

Ser Thr Asp Tyr Tyr Arg Leu Phe Asn Pro Ser Gly Asn Asp Phe  
710 715 720

Cys Ile Trp Cys Glu Val Gly Gly His Thr Met Leu Pro Ile Arg  
725 730 735

Trp Met Pro Pro Glu Ser Ile Met Tyr Arg Lys Phe Thr Thr Glu  
740 745 750

Ser Asp Val Trp Ser Phe Gly Val Ile Leu Trp Glu Ile Phe Thr  
755 760 765

Tyr Gly Lys Gln Pro Trp Phe Gln Leu Ser Asn Thr Glu Val Ile  
770 775 780

Glu Cys Ile Thr Gln Gly Arg Val Leu Glu Arg Pro Arg Val Cys  
785 790 795

Pro Lys Glu Val Tyr Asp Val Met Leu Gly Cys Trp Gln Arg Glu  
800 805 810

Pro Gln Gln Arg Leu Asn Ile Lys Glu Ile Tyr Lys Ile Leu His  
815 820 825

Ala Leu Gly Lys Ala Thr Pro Ile Tyr Leu Asp Ile Leu Gly  
830 835 839

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1858 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGATCCGCGT CGGAGATGGA TGTCTCTCTT TGCCCAGCCA AGTGTAGTTT 50  
CTGGCGGATT TTCTTGCTGG GAAGCGTCTG GCTGGACTAT GTGGGCTCCG 100  
TGCTGGCTTG CCCTGCAAAT TGTGTCTGCA GCAAGACTGA GATCAATTGC 150  
CGGCGGCCGG ACGATGGGAA CCTCTTCCCC CTCCTGGAAG GGCAGGATTC 200  
AGGGAACAGC AATGGGAACG CCAATATCAA CATCACGGAC ATCTCAAGGA 250  
ATATCACTTC CATAACATA GAGAACTGGC GCAGTCTTCA CACGCTCAAC 300  
GCCGTGGACA TGGAGCTCTA CACCGGACTT CAAAAGCTGA CCATCAAGAA 350  
CTCAGGACTT CGGAGCATTG AGCCCAGAGC CTTTGCCAAG AACCCCCATT 400  
TGCGTTATAT AAACCTGTCA AGTAACCGGC TCACCACACT CTCGTGGCAG 450  
CTCTTCCAGA CGCTGAGTCT TCGGGAATTG CAGTTGGAGC AGAACTTTTT 500  
CAACTGCAGC TGTGACATCC GCTGGATGCA GCTCTGGCAG GAGCAGGGGG 550  
AGGCCAAGCT CAACAGCCAG AACCTCTACT GCATCAATGC TGATGGCTCC 600  
CAGCTTCCTC TCTTCCGCAT GAACATCAGT CAGTGTGACC TTCCTGAGAT 650  
CAGCGTGAGC CACGTCAACC TGACCGTACG AGAGGGTGAC AATGCTGTTA 700  
TCACTTGCAA TGGCTCTGGA TCACCCCTTC CTGATGTGGA CTGGATAGTC 750  
ACTGGGCTGC AGTCCATCAA CACTCACCAG ACCAATCTGA ACTGGACCAA 800  
TGTTCAATGCC ATCAACTTGA CGCTGGTGAA TGTGACGAGT GAGGACAATG 850  
GCTTACCCTT GACGTGCATT GCAGAGAACG TGGTGGGCAT GAGCAATGCC 900  
AGTGTGCCC TCACTGTCTA CTATCCCCCA CGTGTGGTGA GCCTGGAGGA 950



GCCTGAGCTG CGCCTGGAGC ACTGCATCGA GTTTGTGGTG CGTGGCAACC 1000  
 CCCCACCAAC GCTGCACTGG CTGCACAATG GGCAGCCTCT GCGGGAGTCC 1050  
 AAGATCATCC ATGTGGAATA CTACCAAGAG GGAGAGATTT CCGAGGGCTG 1100  
 CCTGCTCTTC AACAAAGCCCA CCCACTACAA CAATGGCAAC TATACCCTCA 1150  
 TTGCCAAAAA CCCACTGGGC ACAGCCAACC AGACCATCAA TGGCCACTTC 1200  
 CTCAAGGAGC CCTTTCCAGA GAGCACGGAT AACTTTATCT TGTTTGACGA 1250  
 AGTGAGTCCC ACACCTCCTA TCACTGTGAC CCACAAACCA GAAGAAGACA 1300  
 CTTTTGGGGT ATCCATAGCA GTTGGACTTG CTGCTTTTGC CTGTGTCCTG 1350  
 TTGGTGGTTC TCTTCGTCAT GATCAACAAA TATGGTCGAC GGTCCAAATT 1400  
 TGGAATGAAG GGTCCCGTGG CTGTCATCAG TGGTGAGGAG GACTCAGCCA 1450  
 GCCCACTGCA CCAATCAAC CACGGCATCA CCACGCCCTC GTCACTGGAT 1500  
 GCCGGGCCCC ACACTGTGGT CATTGGCATG ACTCGCATCC CTGTCATTGA 1550  
 GAACCCCCAG TACTTCCGTC AGGGACACAA CTGCCACAAG CCGGACACGT 1600  
 GGGTCTTTTC AAACATAGAC AATCATGGGA TATTAACTT GAAGGACAAT 1650  
 AGAGATCATC TAGTCCCATC AACTCACTAT ATATATGAGG AACCTGAGGT 1700  
 CCAGAGTGGG GAAGTGTCTT ACCCAAGGTC ACATGGTTTC AGAGAAATTA 1750  
 TGTGAATCC AATAAGCCTT CCCGGACATT CCAAGCCTCT TAACCATGGC 1800  
 ATCTATGTTG AGGATGTCAA TGTTTATTTT AGCAAAGGAC GTCATGGCCT 1850  
 TTAAAAAC 1858

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 612 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Asp	Val	Ser	Leu	Cys	Pro	Ala	Lys	Cys	Ser	Phe	Trp	Arg	Ile
1				5				10						15
Phe	Leu	Leu	Gly	Ser	Val	Trp	Leu	Asp	Tyr	Val	Gly	Ser	Val	Leu
			20					25						30
Ala	Cys	Pro	Ala	Asn	Cys	Val	Cys	Ser	Lys	Thr	Glu	Ile	Asn	Cys
			35					40						45

Arg	Arg	Pro	Asp	Asp	Gly	Asn	Leu	Phe	Pro	Leu	Leu	Glu	Gly	Gln	50	55	60
Asp	Ser	Gly	Asn	Ser	Asn	Gly	Asn	Ala	Asn	Ile	Asn	Ile	Thr	Asp	65	70	75
Ile	Ser	Arg	Asn	Ile	Thr	Ser	Ile	His	Ile	Glu	Asn	Trp	Arg	Ser	80	85	90
Leu	His	Thr	Leu	Asn	Ala	Val	Asp	Met	Glu	Leu	Tyr	Thr	Gly	Leu	95	100	105
Gln	Lys	Leu	Thr	Ile	Lys	Asn	Ser	Gly	Leu	Arg	Ser	Ile	Gln	Pro	110	115	120
Arg	Ala	Phe	Ala	Lys	Asn	Pro	His	Leu	Arg	Tyr	Ile	Asn	Leu	Ser	125	130	135
Ser	Asn	Arg	Leu	Thr	Thr	Leu	Ser	Trp	Gln	Leu	Phe	Gln	Thr	Leu	140	145	150
Ser	Leu	Arg	Glu	Leu	Gln	Leu	Glu	Gln	Asn	Phe	Phe	Asn	Cys	Ser	155	160	165
Cys	Asp	Ile	Arg	Trp	Met	Gln	Leu	Trp	Gln	Glu	Gln	Gly	Glu	Ala	170	175	180
Lys	Leu	Asn	Ser	Gln	Asn	Leu	Tyr	Cys	Ile	Asn	Ala	Asp	Gly	Ser	185	190	195
Gln	Leu	Pro	Leu	Phe	Arg	Met	Asn	Ile	Ser	Gln	Cys	Asp	Leu	Pro	200	205	210
Glu	Ile	Ser	Val	Ser	His	Val	Asn	Leu	Thr	Val	Arg	Glu	Gly	Asp	215	220	225
Asn	Ala	Val	Ile	Thr	Cys	Asn	Gly	Ser	Gly	Ser	Pro	Leu	Pro	Asp	230	235	240
Val	Asp	Trp	Ile	Val	Thr	Gly	Leu	Gln	Ser	Ile	Asn	Thr	His	Gln	245	250	255
<del>Thr</del>	<del>Asn</del>	<del>Leu</del>	<del>Asn</del>	<del>Trp</del>	<del>Thr</del>	<del>Asn</del>	<del>Val</del>	<del>His</del>	<del>Ala</del>	<del>Ile</del>	<del>Asn</del>	<del>Leu</del>	<del>Thr</del>	<del>Leu</del>	260	265	270
Val	Asn	Val	Thr	Ser	Glu	Asp	Asn	Gly	Phe	Thr	Leu	Thr	Cys	Ile	275	280	285
Ala	Glu	Asn	Val	Val	Gly	Met	Ser	Asn	Ala	Ser	Val	Ala	Leu	Thr	290	295	300
Val	Tyr	Tyr	Pro	Pro	Arg	Val	Val	Ser	Leu	Glu	Glu	Pro	Glu	Leu	305	310	315
Arg	Leu	Glu	His	Cys	Ile	Glu	Phe	Val	Val	Arg	Gly	Asn	Pro	Pro	320	325	330

Pro Thr Leu His Trp Leu His Asn Gly Gln Pro Leu Arg Glu Ser  
335 340 345

Lys Ile Ile His Val Glu Tyr Tyr Gln Glu Gly Glu Ile Ser Glu  
350 355 360

Gly Cys Leu Leu Phe Asn Lys Pro Thr His Tyr Asn Asn Gly Asn  
365 370 375

Tyr Thr Leu Ile Ala Lys Asn Pro Leu Gly Thr Ala Asn Gln Thr  
380 385 390

Ile Asn Gly His Phe Leu Lys Glu Pro Phe Pro Glu Ser Thr Asp  
395 400 405

Asn Phe Ile Leu Phe Asp Glu Val Ser Pro Thr Pro Pro Ile Thr  
410 415 420

Val Thr His Lys Pro Glu Glu Asp Thr Phe Gly Val Ser Ile Ala  
425 430 435

Val Gly Leu Ala Ala Phe Ala Cys Val Leu Leu Val Val Leu Phe  
440 445 450

Val Met Ile Asn Lys Tyr Gly Arg Arg Ser Lys Phe Gly Met Lys  
455 460 465

Gly Pro Val Ala Val Ile Ser Gly Glu Glu Asp Ser Ala Ser Pro  
470 475 480

Leu His His Ile Asn His Gly Ile Thr Thr Pro Ser Ser Leu Asp  
485 490 495

Ala Gly Pro Asp Thr Val Val Ile Gly Met Thr Arg Ile Pro Val  
500 505 510

Ile Glu Asn Pro Gln Tyr Phe Arg Gln Gly His Asn Cys His Lys  
515 520 525

Pro Asp Thr Trp Val Phe Ser Asn Ile Asp Asn His Gly Ile Leu  
530 535 540

Asn Leu Lys Asp Asn Arg Asp His Leu Val Pro Ser Thr His Tyr  
545 550 555

Ile Tyr Glu Glu Pro Glu Val Gln Ser Gly Glu Val Ser Tyr Pro  
560 565 570

Arg Ser His Gly Phe Arg Glu Ile Met Leu Asn Pro Ile Ser Leu  
575 580 585

Pro Gly His Ser Lys Pro Leu Asn His Gly Ile Tyr Val Glu Asp  
590 595 600

Val Asn Val Tyr Phe Ser Lys Gly Arg His Gly Phe  
605 610 612

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 790 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met	Leu	Arg	Gly	Gly	Arg	Arg	Gly	Gln	Leu	Gly	Trp	His	Ser	Trp	
1				5					10					15	
Ala	Ala	Gly	Pro	Gly	Ser	Leu	Leu	Ala	Trp	Leu	Ile	Leu	Ala	Ser	
				20					25					30	
Ala	Gly	Ala	Ala	Pro	Cys	Pro	Asp	Ala	Cys	Cys	Pro	His	Gly	Ser	
				35					40					45	
Ser	Gly	Leu	Arg	Cys	Thr	Arg	Asp	Gly	Ala	Leu	Asp	Ser	Leu	His	
				50					55					60	
His	Leu	Pro	Gly	Ala	Glu	Asn	Leu	Thr	Glu	Leu	Tyr	Ile	Glu	Asn	
				65					70					75	
Gln	Gln	His	Leu	Gln	His	Leu	Glu	Leu	Arg	Asp	Leu	Arg	Gly	Leu	
				80					85					90	
Gly	Glu	Leu	Arg	Asn	Leu	Thr	Ile	Val	Lys	Ser	Gly	Leu	Arg	Phe	
				95					100					105	
Val	Ala	Pro	Asp	Ala	Phe	His	Phe	Thr	Pro	Arg	Leu	Ser	Arg	Leu	
				110					115					120	
Asn	Leu	Ser	Phe	Asn	Ala	Leu	Glu	Ser	Leu	Ser	Trp	Lys	Thr	Val	
				125					130					135	
Gln	Gly	Leu	Ser	Leu	Gln	Glu	Leu	Val	Leu	Ser	Gly	Asn	Pro	Leu	
				140					145					150	
His	Cys	Ser	Cys	Ala	Leu	Arg	Trp	Leu	Gln	Arg	Trp	Glu	Glu	Glu	
				155					160					165	
Gly	Leu	Gly	Gly	Val	Pro	Glu	Gln	Lys	Leu	Gln	Cys	His	Gly	Gln	
				170					175					180	
Gly	Pro	Leu	Ala	His	Met	Pro	Asn	Ala	Ser	Cys	Gly	Val	Pro	Thr	
				185					190					195	
Leu	Lys	Val	Gln	Val	Pro	Asn	Ala	Ser	Val	Asp	Val	Gly	Asp	Asp	
				200					205					210	
Val	Leu	Leu	Arg	Cys	Gln	Val	Glu	Gly	Arg	Gly	Leu	Glu	Gln	Ala	
				215					220					225	
Gly	Trp	Ile	Leu	Thr	Glu	Leu	Glu	Gln	Ser	Ala	Thr	Val	Met	Lys	
				230					235					240	

Ser Gly Gly Leu	Pro Ser Leu Gly Leu	Thr Leu Ala Asn Val	Thr
245	250		255
Ser Asp Leu Asn Arg	Lys Asn Leu Thr	Cys Trp Ala Glu Asn	Asp
260	265		270
Val Gly Arg Ala	Glu Val Ser Val Gln	Val Asn Val Ser Phe	Pro
275	280		285
Ala Ser Val Gln	Leu His Thr Ala Val	Glu Met His His Trp	Cys
290	295		300
Ile Pro Phe Ser	Val Asp Gly Gln Pro	Ala Pro Ser Leu Arg	Trp
305	310		315
Leu Phe Asn Gly	Ser Val Leu Asn Glu	Thr Ser Phe Ile Phe	Thr
320	325		330
Glu Phe Leu Glu	Pro Ala Ala Asn Glu	Thr Val Arg His Gly	Cys
335	340		345
Leu Arg Leu Asn	Gln Pro Thr His Val	Asn Asn Gly Asn Tyr	Thr
350	355		360
Leu Leu Ala Ala	Asn Pro Phe Gly Gln	Ala Ser Ala Ser Ile	Met
365	370		375
Ala Ala Phe Met	Asp Asn Pro Phe Glu	Phe Asn Pro Glu Asp	Pro
380	385		390
Ile Pro Asp Thr	Asn Ser Thr Ser Gly	Asp Pro Val Glu Lys	Lys
395	400		405
Asp Glu Thr Pro	Phe Gly Val Ser Val	Ala Val Gly Leu Ala	Val
410	415		420
Phe Ala Cys Leu	Phe Leu Ser Thr Leu	Leu Leu Val Leu Asn	Lys
425	430		435
Cys Gly Arg Arg	Asn Lys Phe Gly Ile	Asn Arg Pro Ala Val	Leu
440	445		450
Ala Pro Glu Asp	Gly Leu Ala Met Ser	Leu His Phe Met Thr	Leu
455	460		465
Gly Gly Ser Ser	Leu Ser Pro Thr Glu	Gly Lys Gly Ser Gly	Leu
470	475		480
Gln Gly His Ile	Ile Glu Asn Pro Gln	Tyr Phe Ser Asp Ala	Cys
485	490		495
Val His His Ile	Lys Arg Arg Asp Ile	Val Leu Lys Trp Glu	Leu
500	505		510
Gly Glu Gly Ala	Phe Gly Lys Val Phe	Leu Ala Glu Cys His	Asn
515	520		525

Leu	Leu	Pro	Glu	Gln	Asp	Lys	Met	Leu	Val	Ala	Val	Lys	Ala	Leu	530	535	540
Lys	Glu	Ala	Ser	Glu	Ser	Ala	Arg	Gln	Asp	Phe	Gln	Arg	Glu	Ala	545	550	555
Glu	Leu	Leu	Thr	Met	Leu	Gln	His	Gln	His	Ile	Val	Arg	Phe	Phe	560	565	570
Gly	Val	Cys	Thr	Glu	Gly	Arg	Pro	Leu	Leu	Met	Val	Phe	Glu	Tyr	575	580	585
Met	Arg	His	Gly	Asp	Leu	Asn	Arg	Phe	Leu	Arg	Ser	His	Gly	Pro	590	595	600
Asp	Ala	Lys	Leu	Leu	Ala	Gly	Gly	Glu	Asp	Val	Ala	Pro	Gly	Pro	605	610	615
Leu	Gly	Leu	Gly	Gln	Leu	Leu	Ala	Val	Ala	Ser	Gln	Val	Ala	Ala	620	625	630
Gly	Met	Val	Tyr	Leu	Ala	Gly	Leu	His	Phe	Val	His	Arg	Asp	Leu	635	640	645
Ala	Thr	Arg	Asn	Cys	Leu	Val	Gly	Gln	Gly	Leu	Val	Val	Lys	Ile	650	655	660
Gly	Asp	Phe	Gly	Met	Ser	Arg	Asp	Ile	Tyr	Ser	Thr	Asp	Tyr	Tyr	665	670	675
Arg	Val	Gly	Gly	Arg	Thr	Met	Leu	Pro	Ile	Arg	Trp	Met	Pro	Pro	680	685	690
Glu	Ser	Ile	Leu	Tyr	Arg	Lys	Phe	Thr	Thr	Glu	Ser	Asp	Val	Trp	695	700	705
Ser	Phe	Gly	Val	Val	Leu	Trp	Glu	Ile	Phe	Thr	Tyr	Gly	Lys	Gln	710	715	720
Pro	Trp	Tyr	Gln	Leu	Ser	Asn	Thr	Glu	Ala	Ile	Asp	Cys	Ile	Thr	725	730	735
Gln	Gly	Arg	Glu	Leu	Glu	Arg	Pro	Arg	Ala	Cys	Pro	Pro	Glu	Val	740	745	750
Tyr	Ala	Ile	Met	Arg	Gly	Cys	Trp	Gln	Arg	Glu	Pro	Gln	Gln	Arg	755	760	765
His	Ser	Ile	Lys	Asp	Val	His	Ala	Arg	Leu	Gln	Ala	Leu	Ala	Gln	770	775	780
Ala	Pro	Pro	Val	Tyr	Leu	Asp	Val	Leu	Gly						785	790	

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TGYGAYATHA TGTGGYTNAACAC 23

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TGGATGCARY TNTGGCARCAACA 23

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

YTCRTCYTTN CCRTAYTCRT T 21

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCYTCYTGRATARTAYTCNACGTG 23

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CACGTCAACA ACGGCAACTA CA 22

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GGAAGGATGA GAAACAGATT TCTGC 25

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CATCAATGGC CACTTCCTCA AGG 23

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AGGTGTTTCG TCCTTCTTCT CC 22

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(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GAGATGTGCC CGACCGGTTG TATC 24



(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CACAGTGATA GGAGGTGTGG GA 22

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGATGTGGCT CCAGGCCCC 19

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGGCAACCCG CCCACGGAA 19

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear
- 

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ACGCCAGGCC AAGGGTGAG 19

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: Nucleic Acid

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TAACCACTCC CAGCCCCTGG 20

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TTGGTGGCCT CCAGCGGCAG 20

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AATTCATGAC CACCAGCCAC CA 22

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

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GCTCCTCGGG ACTGCGATGC 20

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATGTCGCCCT GGCCGAGGTG GCAT 24

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AAGCTCAACA GCCAGAACCT C 21

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CAGCTCTGTG AGGATCCAGC C 21

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CCGACCGGTT TTATCAGTGA C 21

(2) INFORMATION FOR SEQ ID NO:31:

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- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATGATCTTGG ACTCCCGCAG AGG 23

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CTTGGCCAAG GCATCTCCGG T 21

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

ATGTGCAGCA CATTAAGAGG A 21

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

TTATACACAG GCTTAAGCCA TCCA 24

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

AGGAGGCATC CAGCGAATG 19

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 9 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Glu Ser Thr Asp Asn Phe Ile Leu Phe  
1 5 9

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Leu Phe Asn Pro Ser Gly Asn Asp Phe Cys Ile Trp Cys Glu  
1 5 10 14

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TCTCCTTCTC GCCGGTGG 18

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Ser Pro Ser Arg Arg Trp  
1 5 6

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Phe Val Leu Phe His Lys Ile Pro Leu Asp Gly  
1 5 10 11

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Trp	Val	Phe	Ser	Asn	Ile	Asp	Asn	His	Gly	Ile	Leu	Asn	Leu	Lys	
1				5					10					15	
Asp	Asn	Arg	Asp	His	Leu	Val	Pro	Ser	Thr	His	Tyr	Ile	Tyr	Glu	
				20					25					30	
Glu	Pro	Glu	Val	Gln	Ser	Gly	Glu	Val	Ser	Tyr	Pro	Arg	Ser	His	
				35					40					45	
Gly	Phe	Arg	Glu	Ile	Met	Leu	Asn	Pro	Ile	Ser	Leu	Pro	Gly	His	
				50					55					60	
Ser	Lys	Pro	Leu	Asn	His	Gly	Ile	Tyr	Val	Glu	Asp	Val	Asn	Val	
				65					70					75	
Tyr	Phe	Ser	Lys	Gly	Arg	His	Gly	Phe							
				80				84							

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